

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2002, 00:35:59 ; Search time 311.51 Seconds
(without alignments)
9882.275 Million cell updates/sec

Title: US-09-719-017a-2
Perfect score: 1793
Sequence: 1 gaattccctgtgacaatta.....caattactcatgcccgcg 1793

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues
Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802.*
1: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
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20: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1793	100.0	1793	21	AAA47190
2	1793	100.0	1793	21	AAZ45325
3	1126.4	62.8	1727	15	AAO86279
4	954.2	53.2	1071	21	AAAI2173
5	404	22.5	5096	16	AAO83824
6	404	22.5	5110	16	AAO83833
7	404	22.5	5110	16	AAO83834
8	404	22.5	5110	16	AAO83835
9	404	22.5	5110	16	AAO83836

10	404	22.5	5110	16	AAO83825	plasmid PCM-X. S
11	404	22.5	5110	16	AAO83826	plasmid PCM-T10-1.
12	404	22.5	5110	16	AAO83827	plasmid PCM-T297.
13	404	22.5	5110	16	AAO83828	plasmid PCM-P1160.
14	404	22.5	5110	16	AAO83829	plasmid PCM-T270.
15	404	22.5	5110	16	AAO83830	plasmid PCM-P1087.
16	404	22.5	5110	16	AAO83831	plasmid PCM-P1198.
17	404	22.5	5110	16	AAO83832	plasmid PCM-T286.
18	403.6	22.5	502	16	AAO92246	trnB ribosomal RNA
19	401.6	22.4	7615	20	AAI18349	Telomerase coding
20	401.6	22.4	7688	20	AAI18351	Telomerase coding
21	401.6	22.4	7797	20	AAI18350	Telomerase coding
22	388.4	21.7	4222	10	AAO92038	Sequence of recomb
23	388.4	21.7	4466	10	AAO90286	ptp104-4 sequence.
24	388.4	21.7	4466	15	AAO58637	ptp104-4 sequence.
25	386.8	21.6	4207	10	AAO92031	Sequence of recomb
26	385.2	21.5	4204	12	AAO10279	Sequence of plasmid
27	336	18.7	5670	22	AAO30800	Vector plasmid pJM
28	336	18.7	5670	22	AAO30801	Vector plasmid pJM
29	336	18.7	5826	22	AAO30798	Vector plasmid pJY
30	336	18.7	6071	22	AAO30799	Vector plasmid pJY
31	332.8	18.6	3753	24	ABA04129	plasmid pHE197(II)
32	332.8	18.6	3755	24	ABA04130	plasmid pHE197(II)
33	332.8	18.6	3950	22	AAO81854	plasmid pSB-92 nuc
34	332.8	18.6	4176	10	AAO90709	Sequence of plasmid
35	332.8	18.6	4214	21	AAO62632	Vector pEP1ink6 D
36	332.8	18.6	4214	21	AAO59260	Nucleotide sequenc
37	332.8	18.6	4357	22	AAO31389	Expression vector
38	332.8	18.6	4816	22	AAO07799	pTRC15B vector co
39	332.8	18.6	5021	21	AAO07775	DNA sequence of pl
40	332.8	18.6	5027	20	AAO78865	Human tissue facto
41	332.8	18.6	5069	20	AAO78874	Human tissue facto
42	332.8	18.6	5069	20	AAO78871	Human tissue facto
43	332.8	18.6	5099	20	AAO78866	Human tissue facto
44	332.8	18.6	5104	22	AAO07798	pTRC15B vector co
45	332.8	18.6	5132	20	AAO78883	Human tissue facto

ALIGNMENTS

RESULT 1	
AAA47190	
ID AAA47190 standard; DNA; 1793 BP.	
XX	
AC AAA47190;	
DT 03-OCT-2000 (first entry)	
DE Nucleotide sequence of the expression cassette of pRPA-BCAT41.	
XX	
KW Methionine; 2-hydroxy-4-methylthiobutanoic acid; nitrilase;	
KW nitrile hydratase; amidase; pRPA-BCAT41; ss.	
XX	
OS Synthetic.	
XX	
FH Key	Location/Qualifiers
FT CDS	123..1193
FT	/*tag= a
XX	
PN WO200036120-A1.	
XX	
PD 22-JUN-2000.	
XX	
PF 10-DEC-1999;	99WO-FR03089.
XX	
PR 11-DEC-1998;	98FR-0015849.
PR 19-JUL-1999;	99FR-0009489.
XX	
PA (RHON) RHONE-POULENC ANIMAL NUTRITION SA.	
XX	
PI Favre-Bulle O, Pierrard J, Batisse Deblitte N;	

DR WPI: 2000-431598/37.
DR P-PSDB: AAV933908.

XX Selecting sequences encoding enzymes involved in methionine synthesis,
PT useful for hydrolysis of nitrile groups, by transforming methionine
PT auxotrophs and selection for growth

Example 1: Page 27-29; 38pp; French.

XX The specification describes a process for the selection and/or isolation
XX of DNA sequences that encode enzymes involved in bioconversion of
CC substrates to methionine or its derivatives such as
CC 2-hydroxy-4-methylthiobutanoic acid. DNA fragments are cloned into
CC a microbial expression vector and recombinant vectors used to transform
CC a host that is auxotrophic for methionine (Met). The cells are cultured
CC in medium containing an adequate amount of substrate and microbes able
CC to grow on this medium are selected and/or isolated. DNA sequences
CC involved in conversion of substrates are then isolated and/or identified.
CC The method is used to identify DNA sequences encoding nitrilases, nitrile
CC hydrolases or amidases. Nitrilases are useful in many synthetic process
CC that require hydrolysis of nitrile groups, e.g. for production of the
CC hydroxy analogue of Met. The present sequence is the nucleotide sequence
CC of the expression cassette of pRPA-BCAT41.

SQ Sequence 1793 BP; 412 A; 527 C; 478 G; 376 T; 0 other;

Query Match 100.0%; Score 1793; DB 21; Length 1793;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1793: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaattccctgttgacaataatcatcgaactagtaactagtagcagcttgctgcaag 60
DB 1 gaattccctgttgacaataatcatcgaactagtaactagtagcagcttgctgcaag 60
QY 61 tgcacctgagcgaagctgggcatcattcaatctgtatctcaaggaattacttac 120
DB 61 tgcacctgagcgaagctgggcatcattcaatctgtatctcaaggaattacttac 120
QY 121 atatgagagaagaataatcgtccggcagcgccgtacagccgcgtctcccaatacag 180
DB 121 atatgagagaagaataatcgtccggcagcgccgtacagccgcgtctcccaatacag 180
QY 181 atcttgcaacgggtgtgtgataaaccattgagctggtctcgaagcccgatgaggct 240
DB 181 atcttgcaacgggtgtgtgataaaccattgagctggtctcgaagcccgatgaggct 240
QY 241 gtagacctgactggtgttgtaaacctggtgccggcctatccctccacgctctgctg 300
DB 241 gtagacctgactggtgttgtaaacctggtgccggcctatccctccacgctctgctg 300
QY 301 ggcgacccggcctgctgcctgaaataacagtcgcgcctactatgccaactgcctcgtg 360
DB 301 ggcgacccggcctgctgcctgaaataacagtcgcgcctactatgccaactgcctcgtg 360
QY 361 acagtgcaaggtttcaacgcatctgcccagcgacgacgacctgtgatttcatcgcac 420
DB 361 acagtgcaaggtttcaacgcatctgcccagcgacgacgacctgtgatttcatcgcac 420
QY 421 tgggttatagcgacgacgacgacgaccttaaccttggtggccaattccgcatcgagaa 480
DB 421 tgggttatagcgacgacgacgacgaccttaaccttggtggccaattccgcatcgagaa 480
QY 481 agggccagatgctgtgtgtcgtcgcgcaaacctcaaacctacacatgcttgagcgacgctgt 540
DB 481 agggccagatgctgtgtgtcgtcgcgcaaacctcaaacctacacatgcttgagcgacgctgt 540
QY 541 tctgtgtaaggttatacgccgagatctgactgtctccgacccgagctggcgctgctgtg 600
DB 541 tctgtgtaaggttatacgccgagatctgactgtctccgacccgagctggcgctgctgtg 600
QY 601 cccctgtgctgcgtgagacccctgtcccttgagcgaagtacgctgtatctcccaacag 660
DB 601 cccctgtgctgcgtgagacccctgtcccttgagcgaagtacgctgtatctcccaacag 660

DB 601 cccctgtgctgcgtgagacccctgtcccttgagcgaagtacgctgtatctcccaacag 660
QY 661 aagccattcaactgtgcgcctggtccgtctcttccgtgtacagcagacagcccatgctgc 720
DB 661 aagccattcaactgtgcgcctggtccgtctcttccgtgtacagcagacagcccatgctgc 720
QY 721 tcagcgccaaggtgaacatgctgtcctcgcaaatctatctcgtgtgaaggccaagtgtcta 780
DB 721 tcagcgccaaggtgaacatgctgtcctcgcaaatctatctcgtgtgaaggccaagtgtcta 780
QY 781 ccatcgccgcagcaatgtcgttaccacgaagagacatgtgacatgctgggaagtgtgaac 840
DB 781 ccatcgccgcagcaatgtcgttaccacgaagagacatgtgacatgctgggaagtgtgaac 840
QY 841 acaacgctccctgcgtgaaagtgtgcggcgagcttcattgatttttgcgcgagagac 900
DB 841 acaacgctccctgcgtgaaagtgtgcggcgagcttcattgatttttgcgcgagagac 900
QY 901 gcaattgtctccctacatctgcacacgatatgcgaaggtcgtatcatcttgccggaagac 960
DB 901 gcaattgtctccctacatctgcacacgatatgcgaaggtcgtatcatcttgccggaagac 960
QY 961 tggagaataattgctcttcgcgaagcgatcaaacctctgtggccactactccaaacccg 1020
DB 961 tggagaataattgctcttcgcgaagcgatcaaacctctgtggccactactccaaacccg 1020
QY 1021 aggcaccccgctctgtgactggaactgtggcgacccgttgagcccaatgactcgtatcca 1080
DB 1021 aggcaccccgctctgtgactggaactgtggcgacccgttgagcccaatgactcgtatcca 1080
QY 1081 aaagcgtgatccaggaagaagctcccgagccgacgctgcaaaagtagctgtgcgccgtcg 1140
DB 1081 aaagcgtgatccaggaagaagctcccgagccgacgctgcaaaagtagctgtgcgccgtcg 1140
QY 1141 ccgtcagcagactcagagctcgatcgtactgtgtgcaagaacccgtctgcaccccaaa 1200
DB 1141 ccgtcagcagactcagagctcgatcgtactgtgtgcaagaacccgtctgcaccccaaa 1200
QY 1201 agatgacaaggcccgycgcaaatctgctcgggtctgattctctctcgtcgtcccgatccact 1260
DB 1201 agatgacaaggcccgycgcaaatctgctcgggtctgattctctctcgtcgtcccgatccact 1260
QY 1261 agttctagaagtcgaactctgcagcagatgcaagcttgggtccactctgaccccaatgacgaact 1320
DB 1261 agttctagaagtcgaactctgcagcagatgcaagcttgggtccactctgaccccaatgacgaact 1320
QY 1321 cagaagtgaacgcgttagcgcgcgactgtgtagtctgggtctcccaatgcaaggttagga 1380
DB 1321 cagaagtgaacgcgttagcgcgcgactgtgtagtctgggtctcccaatgcaaggttagga 1380
QY 1381 actgcagagcatcaataataaagcaaggtcagtcgaagaagctgggacctgtttatc 1440
DB 1381 actgcagagcatcaataataaagcaaggtcagtcgaagaagctgggacctgtttatc 1440
QY 1441 tgttgttttgcgtgaaagctctcctcgtgagttagaacaatcccgccggagacggtttgaac 1500
DB 1441 tgttgttttgcgtgaaagctctcctcgtgagttagaacaatcccgccggagacggtttgaac 1500
QY 1501 gttgcgaagcaaacggtcgggaggtgtgcggcagcgacgcccgcacataaactgcgaagcat 1560
DB 1501 gttgcgaagcaaacggtcgggaggtgtgcggcagcgacgcccgcacataaactgcgaagcat 1560
QY 1561 caaatlaagcagaagcscalcctcgtagcgtatggccttttgcgtttctacaaactctcct 1620
DB 1561 caaatlaagcagaagcscalcctcgtagcgtatggccttttgcgtttctacaaactctcct 1620
QY 1621 gtcgttatattacaagcattcccccacagataacgtaactagcctgttttgcac 1680
DB 1621 gtcgttatattacaagcattcccccacagataacgtaactagcctgttttgcac 1680
QY 1681 aggaagcaggttataagcaactccttaaaacccctggaacacatctggcaatggatcatt 1740
DB 1681 aggaagcaggttataagcaactccttaaaacccctggaacacatctggcaatggatcatt 1740

OY 1741 gctcagacattgtatgtgcgaagacgacacaattactcaatgcccgcg 1793
|||||
Db 1741 gctcagacattgtatgtgcgaagacgacacaattactcaatgcccgcg 1793

RESULT 2
ID AAZ45325 standard; DNA: 1793 BP.
XX AAZ45325;
XX
XX 27-MAR-2000 (first entry)
XX
XX Nucleotide sequence of an expression cassette encoding a nitrilase.
XX
XX Tryptophan promoter; P1rp promoter; heterologous protein expression;
KM Escherichia coli W; Industrial protein production; enzyme: nitrilase; ss.
XX
XX Synthetic.
OS Alcaligenes faecalis.
XX
XX Key Location/Qualifiers
FH CDS 123..1193
FT /*tag= a
FT /product= "nitrilase"
XX
XX MO9964607-A1.
XX
XX 16-DEC-1999.
XX
XX 08-JUN-1999; 99MO-FR01343.
XX
XX 10-JUN-1998; 98FR-0007474.
XX
XX (RHON) RHONE-POULENC NUTRITION ANIMALE.
XX
XX Pierrard J, Guitton C, Favre-Bulle O;
XX
XX WPI: 2000-097541/08.
DR P-PSDB: AA154121.
XX
XX Industrial production of heterologous proteins in Escherichia coli
PT strain W, particularly for expressing enzymes -
XX
XX Example 1: Page 36-38; 52pp: French.
XX
XX The present sequence represents an expression cassette comprising
CC the tryptophan promoter (P1rp promoter) and DNA encoding an Alcaligenes
CC faecalis ATCC8750 nitrilase (nitb). The nitrilase polynucleotide and the
CC promoter sequence were extracted from plasmid pRPA6BcAT6 by restriction
CC digest. The P1rp promoter is used to control the expression of a
CC heterologous protein in an expression cassette which is used to modify
CC a strain of Escherichia coli W. The modified strain is then used for
CC industrial production of heterologous proteins. Specifically, the
CC promoter is used to control the expression of an Alcaligenes nitrilase
CC gene. The method is especially used to produce proteins of relatively
CC low value, preferably enzymes and specifically nitrilases.
XX
XX Sequence 1793 BP: 412 A; 527 C; 478 G; 376 T; 0 other;

Query Match 100.0%; Score 1793; DB 21: Length 1793;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1793: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gattcccggttgacaattatcatcgaactagttaactagtacgagcttgctgcag 60
|||||
Db 1 gattcccggttgacaattatcatcgaactagttaactagtacgagcttgctgcag 60

OY 61 tcgacctgcagccaagcttggtgacatacatcaatcgttatcctaaagaaatactac 120
|||||
Db 61 tcgacctgcagccaagcttggtgacatacatcaatcgttatcctaaagaaatactac 120

OY 121 atatgcagacaagaataaataatcgtccgggcaagccgcgttaacaggccgcctctcccaactacg 180
|||||
Db 121 atatgcagacaagaataaataatcgtccgggcaagccgcgttaacaggccgcctctcccaactacg 180

OY 181 atctgcacaagcgtgtgtgaataaacattgaagctgctcgttcgaagccgcgtgaagaagct 240
|||||
Db 181 atctgcacaagcgtgtgtgaataaacattgaagctgctcgttcgaagccgcgtgaagaagct 240

OY 241 gtgacctgatacgtgtgtgtgaataaaccttgctccgcgtatcccttccacgtcttgctg 300
|||||
Db 241 gtgacctgatacgtgtgtgtgaataaaccttgctccgcgtatcccttccacgtcttgctg 300

OY 301 ggcgaccgctggttcgctggaataatagatgcccgcgtactatcccaactgcgtctctg 360
|||||
Db 301 ggcgaccgctggttcgctggaataatagatgcccgcgtactatcccaactgcgtctctg 360

OY 361 acagtcgaagatlttaacgcatltgcccgaagccgcgacgaccttggttatctcatcgacac 420
|||||
Db 361 acagtcgaagatlttaacgcatltgcccgaagccgcgacgaccttggttatctcatcgacac 420

OY 421 tgggttatagcagagcgagcgagcgagccttacccttggtgccaatgctgtatctgcagaca 480
|||||
Db 421 tgggttatagcagagcgagcgagcgagccttacccttggtgccaatgctgtatctgcagaca 480

OY 481 agggccagatgctgt 540
|||||
Db 481 agggccagatgctgt 540

OY 541 ttgtgaaggttatgtccgagatctgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600
|||||
Db 541 ttgtgaaggttatgtccgagatctgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600

OY 601 cccctgtgtctgt 660
|||||
Db 601 cccctgtgtctgt 660

OY 661 aagccatcacattgtgcgctgtgcgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 720
|||||
Db 661 aagccatcacattgtgcgctgtgcgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 720

OY 721 tcagcccaaggttgacaatgagctgtgccttcgcaaatcattcgtgttgaaagccagtgctta 780
|||||
Db 721 tcagcccaaggttgacaatgagctgtgccttcgcaaatcattcgtgttgaaagccagtgctta 780

OY 781 ccatgcgcgcagcaagtgctgt 840
|||||
Db 781 ccatgcgcgcagcaagtgctgt 840

OY 841 acaagcctccctgtcgtgaagtggt 900
|||||
Db 841 acaagcctccctgtcgtgaagtggt 900

OY 901 gcaatgtgtcctcctaccctgcgcaacagatgacgagccttgatcattgcgcgtatgaaca 960
|||||
Db 901 gcaatgtgtcctcctaccctgcgcaacagatgacgagccttgatcattgcgcgtatgaaca 960

OY 961 tggagaanaatlgccttcgcgcaagcgatcaacgacctgttggtgccaactaccacaacccg 1020
|||||
Db 961 tggagaanaatlgccttcgcgcaagcgatcaacgacctgttggtgccaactaccacaacccg 1020

OY 1021 aagccacccgctgt 1080
|||||
Db 1021 aagccacccgctgt 1080

OY 1081 aaagcgtgtatccagaagaagctcccgagccgacgttgcaaaagttaagcgtgcgcccgtcg 1140
|||||
Db 1081 aaagcgtgtatccagaagaagctcccgagccgacgttgcaaaagttaagcgtgcgcccgtcg 1140

OY 1141 ccgttcagccaagctcagagctcggatagctactgtgtgcaaaagccgtcttgaccacaa 1200
|||||
Db 1141 ccgttcagccaagctcagagctcggatagctactgtgtgcaaaagccgtcttgaccacaa 1200

Db 1083 cacatttgctcctactcgtccacacgatlgcgaagcctgatacttgcgatctgaacat 1142
Qy 962 ggaagaatttgcttcgccaagcgatcaagacctgtggccactactccaaccga 1021
Db 1143 ggaagaatttgcttcgccaagcgatcaagacctgtggccactactccaaccga 1202
Qy 1022 ggcacccgtctgttaactggagaccttggacacgttgaacccatgaactcgtgtatccaa 1081
Db 1203 ggcacccgtctgttaactggagaccttggacacgttgaacccatgaactcgtgtatccaa 1262
Qy 1082 aagcgtgatccagaagaagactcccgagcgcaactgtcaaaagtacggtcgcgcgttcgc 1141
Db 1263 aagcgtgatccagaagaagactcccgagcgcaactgtcaaaagtacggtcgcgcgttcgc 1322
Qy 1142 cgtacgacagactcaagactcgtgatacgtactgtgtcaagaacacgttcctgaaccctcaaa 1201
Db 1323 cgtacgacagactcaagactcgtgatacgtactgtgtcaagaacacgttcctgaaccctcaaa 1382
Qy 1202 gatgacaagcgccgggaactgttcgggttctgtatcttccttcgttcgcggaatcc 1257
Db 1383 gatgacaagcgccgggaactgttcgggttctgtatcttccttcgttcgcggaatcc.1438

RESULT 4

AA12173

ID AA12173 standard; DNA: 1071 BP.

AC AA12173;

DT 10-AUG-2000 (first entry)

DE A. faecalis nitrilase DNA.

KM Nitrilase: chiral carboxylic acid: racemic nitrile: pharmaceutical;

KW plant protection agent; ds:

OS Alcaligenes faecalis.

PN DE19848129-A1.

PD 20-APR-2000.

PF 19-OCT-1998; 98DE-1048129.

PR 19-OCT-1998; 98DE-1048129.

PA (BADI) BASF AG.

PI Rees-Loeschke M, Friedrich T, Hauer B, Mattes R, Engels D;

DR WPI: 2000-319322/28.

P-PSDB; AA187649.

XX New nucleic acid sequence encoding Alcaligenes faecalis nitrilase
PT polypeptide useful for converting racemic nitriles to chiral carboxylic
PR acids

PS Claim 1a: Page 14-16; 28pp; German.

XX This invention describes a novel nucleic acid sequence (I) encoding an
CC Alcaligenes faecalis nitrilase polypeptide. The polypeptide encoded by
CC (I), or a growing, resting or digested microorganism containing (I) is
CC useful for preparing chiral carboxylic acids (III) by conversion of
CC racemic nitriles (IV). (III) are useful as intermediates, e.g. for
CC pharmaceuticals and plant protection agents. This sequence encodes the
CC Alcaligenes faecalis nitrilase described in the method of the invention.

SO Sequence 1071 BP: 230 A; 318 C; 304 G; 219 T; 0 other;

Query Match 53.2%; Score 954.2; DB 21; Length 1071;
Best Local Similarity 93.2%; Pred. No. 5.4e-197;
Matches 998; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 123 atgcagacaagaataatcgtccggcagccgcgtacagagccgcgtctcccaactacgat 182
Db 1 atgcagacaagaataatcgtccggcagccgcgtacagagccgcgtctcccaactacgat 60
Qy 183 ctgcgaacgggtgtgttgaataaacatctagctgtgtctcagggcccgatgaaggcgt 242
Db 61 ctgcgaacgggtgtgttgaataaacatctagctgtgtctcagggcccgatgaaggcgt 120
Qy 243 gacctgaatcgttgttgtgaaaccttgctgcccgtctatcccttccacgtctgtgtggc 302
Db 121 gacctgaatcgttgttgtgaaaccttgctgcccgtatacccttccacgtctgtgtggc 180
Qy 303 gcaacggccttgctgtcgtgaataacagctccgcgtactatgtccaactcgtctgtgtgac 362
Db 181 gcaacggccttgctgtcgtgaataacagctccgcgtactatgtccaactcgtctgtgtgac 240
Qy 363 atgcagagtttcaacgcatctgcccagcgcaagcagaccttggtatcttcaatcgtcgt 422
Db 241 atgcagagtttcaacgcatctgcccagcgcaagcagaccttggtatcttcaatcgtcgt 300
Qy 423 ggtataagcagcgcagcgcgcgcgttcaacttggtgccaatgctgtatcgacgacaag 482
Db 301 ggtataagcagcgcagcgcgcgttcaacttggtgccaatgctgtatcgacgacaag 360
Qy 483 ggcacagatcgtgtgtgtcgtcgttcgcaaaactcaacatcaatgttgacgcgacgtgtt 542
Db 361 ggcacagatcgtgtgtgtcgtcgttcgcaaaactcaacatcaatgttgacgcgacgtgtt 420
Qy 543 ggtgaaggtatgtcccgagatctgattgtgttcgcaacagcagctggcgcgctgtgtcc 602
Db 421 ggtgaaggtatgtcccgagatctgattgtgtgttcgcaacagcagctggcgcgctgtgtcc 480
Qy 603 ctgtgtcgtcgtggagacactgtcccttgagcaaatcgcgtgttaactccagcagaa 662
Db 481 ctgtgtcgtcgtggagacactgtcccttgagcaaatcgcgtgttaactccagcagaa 540
Qy 663 gccatccaatctgcgcgtcgttcgttcgttcgtaacaggaacgacatcgtcgtc 722
Db 541 gccatccaatctgcgcgtcgttcgttcgttcgtaacaggaacgacatcgtcgtc 600
Qy 723 agcgccaaggtgacaatctgctccctcgcaaatctatctcgttgaagcgagtgcttacc 782
Db 601 agtgccaaggtgacaatctgctccctcgcaaatctatctcgttgaagcgagtgcttacc 660
Qy 783 atcgcgcgcagcagtgctgtcaaccgaagagacatgacatgtgtgaagtgaagacac 842
Db 661 atcgcgcgcagcagtgctgtcaaccgaagagacatgacatgtgtgaagtgaagacac 720
Qy 843 aacgctcccttgctgaagaagtgtggcgcgcgatcttccatgattttgcccgcgagcagc 902
Db 721 aacgctcccttgctgaagaagtgtggcgcgcgatcttccatgattttgcccgcgagcagc 780
Qy 903 acatgtgctcccttaccctccacacgactgcgaagcgccgatcatctgcccagatgacatg 962
Db 781 acatgtgctcccttaccctccacacgactgcgaagcgccgatcatctgcccagatgacatg 840
Qy 963 gaagaatttgcttcgccaagcgataacgacacctgtgtggccactactccaaccgag 1022
Db 841 gaagaatttgcttcgccaagcgataacgacacctgtgtggccactactccaaccgag 900
Qy 1023 gccacccgtctgtgtactgtgactgtggacacgttgagcccatgactcgggttgatccaa 1082
Db 901 gccacccgtctgtgtactgtgactgtggacacgttgagcccatgactcgggttgatccaa 960
Qy 1083 agcgtgatccaagaagactcccgagcgcaacgctgcaaaagtacggcgtcgccgtcc 1142
Db 961 agcgtgatccaagaagactcccgagcgcaacgctgcaaaagtacggcgtcgccgtcc 1020
Qy 1143 gtcagccagactcaggaactcgtatcgtgtgtcaagaacgctcctga 1193
Db 1021 atcagcactccacaggaactcgtatcgtgtgtcaagaacgctcctga 1071

ID	AAQ83824	standard: DNA: 5096 BP.
AC	AAQ83824;	
DT	04-OCT-1995	(first entry)
DE	Plasmid pKK232-8.	
KM	Plasmid pKK232-8; bacteriophage T7; RNA polymerase;	
KW	mutant promoters; circular; cycIIc; ds.	
OS	Synthetic.	
FT	Key	Location/Qualifiers
FT	misc_feature	177..212
FT	/*tag=	a
FT	/note=	"Cloning polylinker prior to a promoterless chloramphenicol acetyl transferase gene"
PN	US5385834-A.	
XX	31-JAN-1995.	
XX	13-AUG-1993;	93US-0106433.
XX	13-AUG-1993;	93US-0106433.
XX	(GEOR-) GEORGIA TECH RES CORP.	
PI	Ikedai RA;	
DR	WPI; 1995-081565/11.	
PT	New mutant form of T7 RNA polymerase - able to utilise a wide	
PT	range of T7 promoter sequences having mutations that inactivate	
PT	recognition by wild type enzyme	
PS	Disclosure: Columns 37-42: 79pp; English.	
CC	AA083824 is the plasmid pKK232-8, it was used in the production of	
CC	claimed bacteriophage T7 RNA polymerase mutant promoters.	
XX	Sequence 5096 BP: 1294 A; 1290 C; 1290 G; 1222 T; 0 other;	
SO		
Query Match	22.5%;	Score 404; DB 16; Length 5096;
Best Local Similarity	96.5%;	Pred. No. 4.9e-78;
Matches 413; Conservative	0;	Mismatches 15; Indels 0; Gaps 0;
QY	1267 agagtcgacgtcgaagcatgcaagctctggtccacgtgaccacatgcccgaactcagaag	1326
DB	1237 agaatcttgcttgccgagcagtagcgggtgtgtccacgtgaccacatgcccgaactcagaag	1296
QY	1327 tgaaacgcgttagcgccgagctgtagtctgtgggtctcccatgagagtagtgaagactgcc	1386
DB	1297 tgaaacgcgttagcgccgagctgtagtctgtgggtctcccatgagagtagtgaagactgcc	1356
QY	1387 aggcgtcaataataaagcgaagagctcagtcgaaagagctgggcttctgtttatctgtgt	1446
DB	1357 aggcgtcaataataaagcgaagagctcagtcgaaagagctgggcttctgtttatctgtgt	1416
QY	1447 tctgtcgttcaacgctctccctgagtaggagcaaatcccgccggagcgagatttgaagcttgcg	1506
DB	1417 tctgtcgttgaagagctctccctgagtaggagcaaatcccgccggagcgagatttgaagcttgcg	1476
QY	1507 aagcaacggcccgaggggtgtgctggcagaagcgcgcgcacataaactgtccagagcatcaat	1566
DB	1477 aagcaacggcccgaggggtgtgctggcagaagcgcgcgcacataaactgtccagagcatcaat	1536
QY	1567 aagcagaagggccatctctgaacgtagtggccttttgcgtttctacaacatcttccgtgtgc	1626

Dd	1537	aagcagaaggccatccctgcgagtagggccttcttgctttccaacacttcctgtcgcc	1596
Qy	1627	atatctacaagccattcccccccacaatacgaatacgttaaacctagacctgttttgcatlcaggaaa	1686
Dd	1597	atatctacaagccattcccccccacaatacgaatacgttaaacctagacctgttttgcatlcaggaaa	1656
Qy	1687	gcagcttat	1694
Dd	1657	gcagcttgt	1664
<hr/>			
Result 6			
AA083833			
ID	AA083833	standard; DNA; 5110 BP.	
XX			
AC	AA083833;		
DT			
XX	05-OCT-1995	(first entry)	
DE			
XX	Plasmid pcm-B64.		
XX			
KW	Plasmid pcm-B64; bacteriophage T7; RNA polymerase;		
KM	mutant -8T to C; T7 promoter phi 10; circular; cyclIc; ds.		
XX			
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	Promoter	198..220	
FT		/+tag= "A"	
FT		/note= "intermediate T7 promoter phi 10 mutant (-8T to C) prior to a promoterless chloramphenicol acetyl transferase gene"	
XX			
FN	US5385834-A.		
PD	31-JAN-1995.		
XX			
PF	13-AUG-1993;	93US-0106433.	
XX			
PR	13-AUG-1993;	93US-0106433.	
XX			
PA	(GEOR-) GEORGIA TECH RES CORP.		
PI	Ikedra RA;		
DR	WPI; 1995-081565/11.		
XX			
PT	New mutant form of T7 RNA polymerase - able to utilise a wide range of T7 promoter sequences having mutations that inactivate recognition by wild type enzyme		
PS	Disclosure: Columns 97-104; 79pp; English.		
CC	AA083833 is the plasmid PCM-B64, it was used in the production of the bacteriophage T7 RNA polymerase mutant promoter phi 10 -8T to C substitution (claimed).		
CC			
XX	Sequence 5110 BP; 1305 A; 1289 C; 1289 G; 1227 T; 0 other;		
<hr/>			
Query Match 22.5%; Score 404; DB 16; Length 5110; Best Local Similarity 96.5%; Pred. No. 4.9e-78; Matches 413; Conservative 0; Mismatches 15; Indels 0; Gaps 0;			
Dd	1267	aaagtcgacctgcagagcatagcgaagcttgggtctccaccctgaccccaatgcgcgaactcagaag	1326
Dd	1251	agaatttcgctggcgagcagtagcgggctgtctccaccctgaccccaatgcgcgaactcagaag	1310
Qy	1327	tbaaacgccgatgcagcccgatgtgtatgttggtgtctcccatgcagagtagaggaactgcc	1386
Dd	1311	tgaaacgccgatgcagccgatgtgtatgttggtgtctcccatgcagagtagaggaactgcc	1370

XX	AAO83834 standard; DNA: 5110 BP.
XX	AAO83834:
XX	05-OCT-1995 (first entry)
XX	Plasmid pcm-p1208.
XX	Plasmid pcm-p1208; bacteriophage T7; RNA polymerase;
KW	mutant -7C to G; T7 promoter phi 10; circular; cyclic; ds.
XX	Synthetic.
OS	
XX	Key
FH	Location/Qualifiers
FT	Promoter 198..220
FT	/tag= a
FT	/note= "inactive T7 promoter phi 10 mutant (-7C to
FT	G) prior to a promoterless chloramphenicol
FT	acetyl transferase gene"
PN	US5385834-A.
XX	
PD	31-JAN-1995.
XX	
XX	13-AUG-1993; 93US-0106433.
PP	
XX	
PR	13-AUG-1993; 93US-0106433.
XX	
PA	(GEOR-) GEORGIA TECH RES CORP.
XX	
PI	Ikedo RA;
XX	
DR	WPI: 1995-081565/11.
XX	
PT	New mutant form of T7 RNA polymerase - able to utilise a wide
PT	range of T7 promoter sequences having mutations that inactivate
PT	recognition by wild type enzyme
XX	
PS	Disclosure; Columns 105-110; 79pp; English.
XX	
CC	AAO83834 is the plasmid pcm-p1208, it was used in the production of
CC	the bacteriophage T7 RNA polymerase mutant promoter phi 10 -7C
CC	to G substitution (claimed).
XX	
XQ	Sequence 5110 BP; 1305 A; 1288 C; 1290 G; 1227 T; 0 other;

QY	1267	agagtcgacctgcagcgatctgcaagcttgggtctccaaacttbaaccatctgcgaactcagaag	1326
Db	1251	aggaattcgcttcgctgcggaatgacgcgcggtggtctccacctgaaacctcattgcgaactcagaag	1310
QY	1327	tgaacgcgcgtaagcgcgcgaatgtagtgttggtgtctctcccatctgaaagttagggaaacttgcc	1386
Db	1311	tgaacgcgcgtaagcgcgcgaatgtagtgttggtgtctctcccatctgaaagttagggaaacttgcc	1370
QY	1387	agagatcaaatataaacgaaagagctcaagctcgaaaagacttgggccttctcgtttatctgtgtgt	1446
Db	1371	agagatcaaatataaacgaaagagctcaagctcgaaaagacttgggccttctcgtttatctgtgtgt	1430
QY	1447	ttgtcgtgtgaacgctcttcctcgatgaagacaatactccgcgcggaagcgatttgaacgttgcg	1506
Db	1431	ttgtcgtgtgaacgctcttcctcgatgaagacaatactccgcgcggaagcgatttgaacgttgcg	1490
QY	1507	aagcaacgcgcgcgcggaaggttggtgcgcgcgaagacgcgcgcgcataaacttgcagaagcatcaatt	1566
Db	1491	aagcaacgcgcgcgcggaaggttggtgcgcgcgaagacgcgcgcgcataaacttgcagaagcatcaatt	1550
QY	1567	aagcaagaagggccatctcctgaacgagtagtcctttttgctttctcaaaccttctccgttgctc	1626
Db	1551	aagcaagaagggccatctcctgaacgagtagtcctttttgctttctcaaaccttctccgttgctc	1610
QY	1627	atactctcaagccatccccccacagataacgtaaacatagcctcgtttttgtcatcaggaata	1686
Db	1611	atactctcaagccatccccccacagataacgtaaacatagcctcgtttttgtcatcaggaata	1670
QY	1687	gcagactat 1694	
Db	1671	gcagactgt 1678	

RESULT	8
AAQ83835	
ID	AAQ83835 standard; DNA; 5110 BP.
XX	
AC	AAQ83835;
XX	
DT	06-OCT-1995 (first entry)
XX	
DE	Plasmid PCM-P1031.
XX	
KW	Plasmid PCM-P1031; bacteriophage T7; RNA polymerase;
KW	mutant -7C to A; T7 promoter Ph1 I0; circular; cyclic; ds.
XX	
OS	Synthetic.
XX	
EH	Key
FT	Location/Qualifiers
FT	Promoter
FT	198..220
FT	/*tag= a
FT	/note= "inactive T7 promoter phi 10 mutant (-7C to
FT	A) prior to a promoterless chloramphenicol
FT	acetyl transferase gene"
XX	
PN	US5385834-A.
XX	
PD	31-JAN-1995.
XX	
PP	13-AUG-1993; 93US-0106433.
XX	
PR	13-AUG-1993; 93US-0106433.
XX	
PA	(GEOR-) GEORGIA TECH RES CORP.
XX	
PI	Ikeda RA;
XX	
DR	WPI; 1995-081565/11.

Query Match	22.5%	Score 404	DB 16	Length 5110
Best Local Similarity	96.5%	Pred. No. 4.9e-78		
Matches 413	Conservative	0	Mismatches 15	Indels 0
				Gaps 0

	RESULT	9
AA083836		
ID	AA083836	standard; DNA; 5110 BP.
XX		
AC	AA083836;	
XX		
DT	06-Oct-1995	(first entry)
XX		
DE	Plasmid pCM-T221.	
XX		
KW	Plasmid pCM-T221; bacteriophage T7; RNA polymerase;	
KW	mutant -6A to G; T7 promoter pM110; circular; cyclic; ds	
XX		
OS	Synthetic.	

FH	Key	Location/Qualifiers
FT	Promoter	198..220
FT		/*tag=
FT		/note=
FT		"intermediate T7 promoter phi 10 mutant (-6A
FT		to 6)" prior to a promoterless chloramphenicol
XX		acetyl transferase gene"

Query Match	22.5%	Score 404	DB 16	Length 5110
Best Local Similarity	96.5%	Pred. No. 4.9e-78		
Matches 413, Conservative	0	Mismatches 15	Indels 0	Gaps 0

[illegible]

RESULT 10	
ID	AAQ83825 standard; DNA: 5110 BP
XX	AAQ83825
AC	AAQ83825;
XX	
DT	04-Oct-1995 (first entry)
XX	
DE	Plasmid PCM-X#.

	Query Match	92.5%	Score 404	DB 16:	Length 5110:	
	Best Local Similarity	96.5%:	Pred. No. 4.9e-78:			
	Matches 413:	Conservative 0:	Mismatches 15:	Indels 0:	Gaps 0:	
OY	1267 agagtcgacctgcaggcatgtcaagcttggltccaccctgaaccacctgcgaactcagaag	1326				
Db	1251 agaatttccttgscgtagcggtggtctccacctgaaccatgccgaactcagaag	1310				
OY	1327 tgaacgcgcgtagcgcgcgatgtgtgtgtgtgtttccccatgctgagagttaggaactgcc	1386				
Db	1311 tgaaacgcgcgttagcgcgatgtgtgtgtgtgtgtttccccatgctgagagttaggaactgcc	1370				
OY	1387 aggcatacaataaaacgaaaggctcagtcgaaagactggccttcgatttatctgtgt	1446				
Db	1371 aggcatacaataaaacgaaaggctcagtcgaaagactggccttcgatttatctgtgt	1430				
OY	1447 ttgtcgtgtgaacgcgtctctcctgtagtagacaataccgcgcggagcgagatttgaacgttcg	1506				
Db	1431 ttgtcgtgtgaacgcgtctctcctgtagtagacaataccgcgcggagcgagatttgaacgttcg	1490				
OY	1507 aagcagcagcccgcggagggtgtggtggcaggaacgcccgccaataactgfcagagataaat	1566				
Db	1491 aagcagcagcccgcggagggtgtggtggcaggaacgcccgccaataactgfcagagataaat	1550				
OY	1567 aagcaggaagccatctctgcagatgtgccttttttcgltttctaanaacttcctgtcgtc	1626				
Db	1551 aagcaggaagccatctctgcagatgtgccttttttcgltttctaanaacttcctgtcgtc	1610				
OY	1627 atattacaagcattccccccacagatacgttaactagctcgtttttgcatacgaaga	1686				
Db	1611 atattacaagcattccccccacagatacgttaactagctcgtttttgcatacgaaga	1670				
OY	1687 gcaagctat 1694 }					
Db	1671 gcaagcttgt 1678					
RESULT 14						
AAO83829						
ID AAO83829	standard; DNA; 5110 BP.					
XX						
AC AAO83829;						
XX						
DT 04-OCT-1995 (first entry)						
XX						
DE Plasmid PCM-T720.						
XX						
KW Plasmid PCM-T720; bacteriophage T7; RNA polymerase;						
KM mutant -9C to A; T7 promoter phi 10; circular; cyclic; ds.						
XX						
OS Synthetic.						
XX						
FH Key	Location/Qualifiers					
FH Promoter	198..220					
FT /*tag=^a						
FT /note="Inactive T7 promoter phi 10 mutant (-9C to						
FT prior to a promoterless chloramphenicol						
FT acetyl transferase gene"						
XX						
PN US5385834-A.						
XX						
PD 31-JAN-1995.						
XX						
PF 13-AUG-1993; 93US-0106433.						
XX						
PR 13-AUG-1993; 93US-0106433.						
XX						
PA (GEOR-) GEORGIA TECH RES CORP.						
XX						
IKeda RA;						
XX						

DR	WPI: 1995-081565/11.
XX	
PT	New mutant form of T7 RNA polymerase - able to utilise a wide
PT	range of T7 promoter sequences having mutations that inactivate
PT	recognition by wild type enzyme
XX	
PS	Disclosure: Columns 71-76; 79pp; English.
XX	
CC	AA083829 is the plasmid PCM-T7270, it was used in the production of
CC	the bacteriophage T7 RNA polymerase mutant promoter phi 10 -9C
CC	to A substitution (claimed).
XX	
SO	Sequence 5110 BP: 1306 A; 1287 C; 1289 G; 1228 T; 0 other;
	Query Match 22.5%; Score 404; DB 16; Length 5110;
	Best Local Similarity 96.5%; Pred. No. 4.9e-78;
	Matches 413; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY	1267 agagtcgacgtcgcagcatgacagcttgggtccacctgaccccatgccgaactagaag 1326
DB	1251 agaatttgcctgcgcgcagtagcgcgtgtgtcccaactgaccccatgcgaactcagaag 1310
QY	1327 tgaacgcgcgtatgcgcgcagtagtattgtgtgggtctcccatgacgagtaggaactgac 1386
DB	1311 tgaacgcgcgtatgcgcgcagtagtattgtgtgggtctcccatgacgagtaggaactgac 1370
QY	1387 aggcctcaataaaccgaaaggctcagtcgaaagactggccttcgttttctcgttgt 1446
DB	1371 aggcctcaataaaccgaaaggctcagtcgaaagactggccttcgttttctcgttgt 1430
QY	1447 ttgtcgtgtgaacgctctcctctgtagtagacaataccgcgcggagcggattgaacgttcgcg 1506
DB	1431 ttgtcgtgtgaacgctctcctctgtagtagacaataccgcgcggagcggattgaacgttcgcg 1490
QY	1507 aagcaacggtcccgaggggtgtgcgggcaggaagcccgccataactgcgcagcgcataaatt 1566
DB	1491 aagcaacggtcccgaggggtgtgcgggcaggaagcccgccataactgcgcagcgcataaatt 1550
QY	1567 aagcgaagaagccatccctacgcatggccttttgcgtttcttcaaacacttctctgtcgtc 1626
DB	1551 aagcgaagaagccatccctacgcatggccttttgcgtttcttcaaacacttctctgtcgtc 1610
QY	1627 atatacacaagccatccccccacaagatacgtgaaactagcctcgttttgcatacggaaa 1686
DB	1611 atatacacaagccatccccccacaagatacgtgaaactagcctcgttttgcatacggaaa 1670
QY	1687 gcaactat 1694
DB	1671 gcaactgt 1678
	RESULT 15
AC	AA083830 standard; DNA; 5110 BP.
XX	
AC	AA083830;
XX	
DT	05-OCT-1995 (first entry)
XX	
DE	Plasmid PCM-P1087.
XX	
KM	Plasmid PCM-P1087; bacteriophage T7; RNA polymerase;
KW	mutant -9C to T; T7 promoter phi 10; circular; cyclic; ds.
XX	
OS	Synthetic.
XX	
FT	Key Location/Qualifiers
FT	Promoter 198..220
FT	/tag= a
FT	/note= "inactive T7 promoter phi 10 mutant (-9C to
FT	T) prior to a promoterless chloramphenicol
FT	acetyl transferase gene"

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XX US5385834-A.
PN
XX
XX 31-JAN-1995.
PD
XX
XX 13-AUG-1993; 93US-0106433.
PE
XX
XX 13-AUG-1993; 93US-0106433.
PR
XX
XX 13-AUG-1993; 93US-0106433.
PA
XX (GEOR-) GEORGIA TECH RES CORP.
PI Ikeda RA;
XX
XX WPI; 1995-081565/11.
DR
XX
XX New mutant form of T7 RNA polymerase - able to utilise a wide
PT range of T7 promoter sequences having mutations that inactivate
PT recognition by wild type enzyme
XX
XX Disclosure: Columns 77-83; 79pp; English.
PS
XX
XX AA083830 is the plasmid PCM-P1087, it was used in the production of
CC the bacteriophage T7 RNA polymerase mutant promoter phi 10 -9C
CC to T substitution (claimed).
XX
XX Sequence 5110 BP; 1305 A; 1287 C; 1289 G; 1229 T; 0 other;
SQ

Query Match 22.5%; Score 404; DB 16; Length 5110;
Best Local Similarity 96.5%; Pred. No. 4.9e-78;
Matches 413; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1267 agagtcgacctgcaaggatgcaagcttggctccacctgaccccatgccaactcagaag 1326
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1251 agaatttcgctgcgcgtagcgtagcggtgctgcacacccatgccaactcagaag 1310

QY 1327 tgaacgcgcgtatagcgcgatgtatgtgtggtctcccatgagagtaggaaatgcc 1386
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1311 tgaacgcgcgtatagcgcgatgtatgtgtggtctcccatgagagtaggaaatgcc 1370

QY 1387 aggcataataaagcaagagcctcagtcgaaagactggccttcgcttctatctgtgt 1446
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1371 aggcataataaagcaagagcctcagtcgaaagactggccttcgcttctatctgtgt 1430

QY 1447 ttgtcgtgtaacgctctcctcgtatggaacaaatccgcgcggagcggaatttgaacgttcg 1506
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1431 ttgtcgtgtaacgctctcctcgtatggaacaaatccgcgcggagcggaatttgaacgttcg 1490

QY 1507 aagcaacgcccgcggaggtgtggtggcgaagagccgcgcataaactgcagcatcaaat 1566
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1491 aagcaacgcccgcggaggtgtggtggcgaagagccgcgcataaactgcagcatcaaat 1550

QY 1567 aagcagaagccatcctcagcgaatgaccttttgcgttctcacaactcttcgttcgtc 1626
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1551 aagcagaagccatcctcagcgaatgaccttttgcgttctcacaactcttcgttcgtc 1610

QY 1627 atatctacaagccatccccccacagatacgtglaaactagcctcgttttgcatacagaana 1686
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1611 atatctacaagccatccccccacagatacgtglaaactagcctcgttttgcatacagaana 1670

QY 1687 gcaagctat 1694
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1671 gcaagctgt 1678
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Job time: 7667 sec